

STIC-Biotech/ChemLib

159912

119

From: Bowman, Amy
Sent: Wednesday, July 20, 2005 7:05 AM
To: STIC-Biotech/ChemLib
Cc: Bowman, Amy
Subject: sequence search-10/800,487

Hello,

I need a score over length search of GenBank number NM_000201 for application 10/800,487, with lower and upper limits of 18 and 26 nucleotides, and a minimum identity of 80%. I apologize but applicant has not disclosed the sequence by anything other than the GenBank number.

Thank you,
Amy Bowman
AU 1635
REM 2C31
mail-REM 2C18
571-272-0755

STIC
10/20/05
10/20/05

Noble Jarrell

STAFF USE ONLY

Searcher: Noble
Searcher Phone: 2-
Date Searcher Picked up: 7/26/05
Date Completed: 7/26/05
Searcher Prep/Rev. Time: 10
Online Time: 40

Type of Search

NA#: 16 AA#: _____
Interference: _____ SPDI: _____
S/L: ✓ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: Cambridge, seq
WWW/Internet: _____
Other(Specify): _____

SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is 90%.

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.